Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of separately detecting a first and a second RNA isoform from a target gene in an RNA sample comprising:

contacting an RNA sample with random primers under hybridization conditions;

generating cDNA from the RNA sample by extending the random primers with reverse transcriptase to produce cDNA;

degrading the RNA population;

fragmenting the cDNA;

labeling the cDNA fragments;

contacting the labeled cDNA fragments with an array ~~a solid support~~ comprising nucleic acid probes attached to a solid support[[,]] under hybridization conditions, wherein said array comprises a first probe that is perfectly complementary to the first RNA isoform and not to the second RNA isoform and a second probe that is perfectly complementary to the second RNA isoform and not to the first RNA isoform; and

detecting the presence or absence of hybridization of the labeled cDNA fragments to the nucleic acid probes on the solid support.

2. (original) The method of claim 1 wherein, for the majority of RNAs in the starting sample, the number of cDNA copies of a given sequence near the 3' end of a single species of RNA is not more than twice the number of cDNA copies of a given sequence near the 5' end of said single species of RNA.

3. (original) The method of claim 1 wherein said RNA is selected from the group consisting of total RNA, mRNA and poly(A)$^+$ RNA.

4. (original) The method of claim 1 wherein hybridization is detected by detecting a signal from labeled DNA which is hybridized to the solid support.

5. (original) The method of claim 1 wherein the cDNA fragments are labeled by the addition of at least one labeled nucleotide using terminal transferase.

6. (original) The method of claim 4 wherein the signal is amplified.

Claims 7-9 (canceled)

10. (original) The method of claim 1 wherein the solid support comprising nucleic acid probes is selected from the group consisting of a nucleic acid probe array, a membrane blot, a microwell, a bead, and a sample tube.

11. (original) The method of claim 1 wherein the random primers are 6 nucleotides in length.

12. (original) The method of claim 1 wherein the random primers are 9 nucleotides in length.

13. (original) The method of claim 1 wherein the random primers are 15 nucleotides in length.

14. (original) The method of claim 1 wherein the RNA sample is isolated from a prokaryotic cell.

15. (original) The method of claim 1 wherein the RNA sample is isolated from a eukaryotic cell or tissue.

16. (original) The method of claim 15 wherein the eukaryotic cell or tissue is mammalian.

17. (original) The method of claim 16 wherein the eukaryotic cell or tissue is human.

18. (original) The method of claim 1 wherein the RNA sample is isolated from a source selected from the group consisting of dissected tissue, microdissected tissue, a tissue subregion, a tissue biopsy sample, a cell sorted population, a cell culture, and a single cell.

19. (original) The method of claim 1 wherein the RNA sample is isolated from a cell or tissue source selected from the group consisting of brain, liver, heart, kidney, lung, retina, bone, lymph node, endocrine gland, reproductive organ, blood, nerve, vascular tissue, and olfactory epithelium.

20. (original) The method of claim 1 wherein the RNA sample is isolated from a cell or tissue source selected from the group consisting of embryonic and tumorigenic.

21. (original) The method of claim 1 further comprising amplifying the cDNA fragments to produce amplified cDNA fragments.

22. (original) The method of claim 21 further comprising:

contacting said amplified cDNA fragments with a solid support comprising nucleic acid probes.

23. (original) The method of claim 22 further comprising:

detecting the presence or absence of hybridization of said amplified cDNA fragments to the nucleic acid probes on the solid support.

24. (original) The method of claim 23 wherein the solid support is selected from the group consisting of a nucleic acid probe array, a membrane blot, a microwell, a bead, and a sample tube.

25. (original) The method of claim 1 wherein the RNA sample is further contacted with primer comprising poly dT.

26. (original) The method of claim 23 wherein hybridization is detected by detecting a signal from labeled DNA which is hybridized to the solid support.

27. (original) The method of claim 26 wherein the signal is amplified.

28. (original) A gene expression monitoring system comprising the labeled cDNA fragments of Claim 1 and a solid support comprising nucleic acid probes.

29. (original) A gene expression monitoring system comprising the labeled cDNA fragments of Claim 21 and a solid support comprising nucleic acid probes.

Claims 30-40 (canceled)